FIG. 1

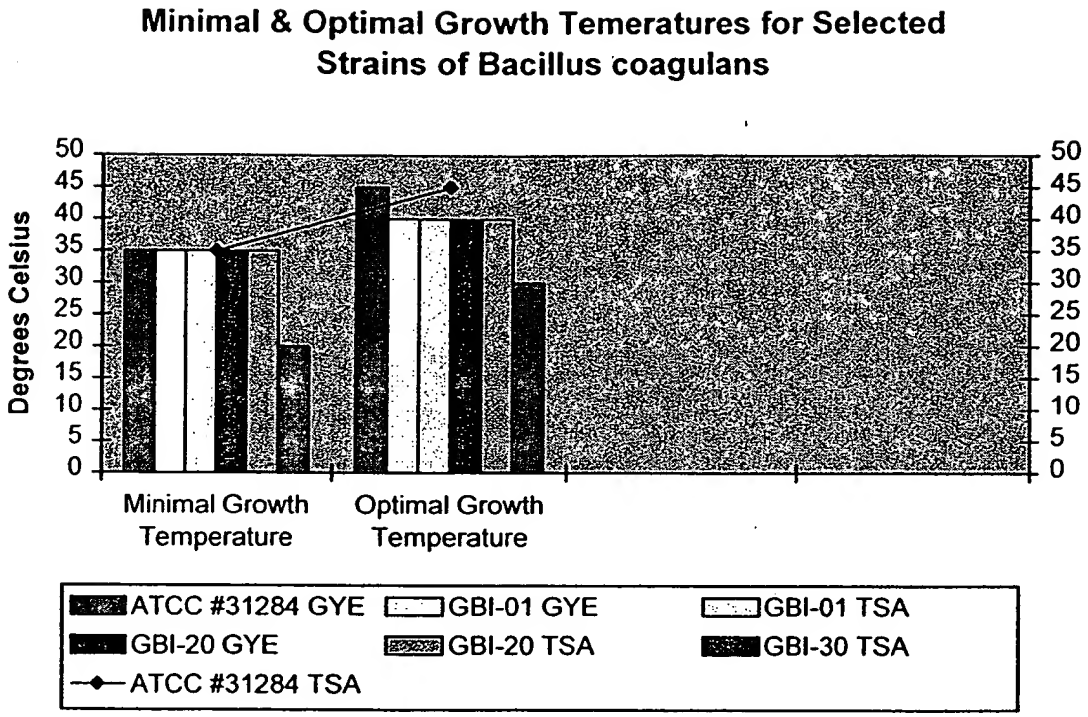
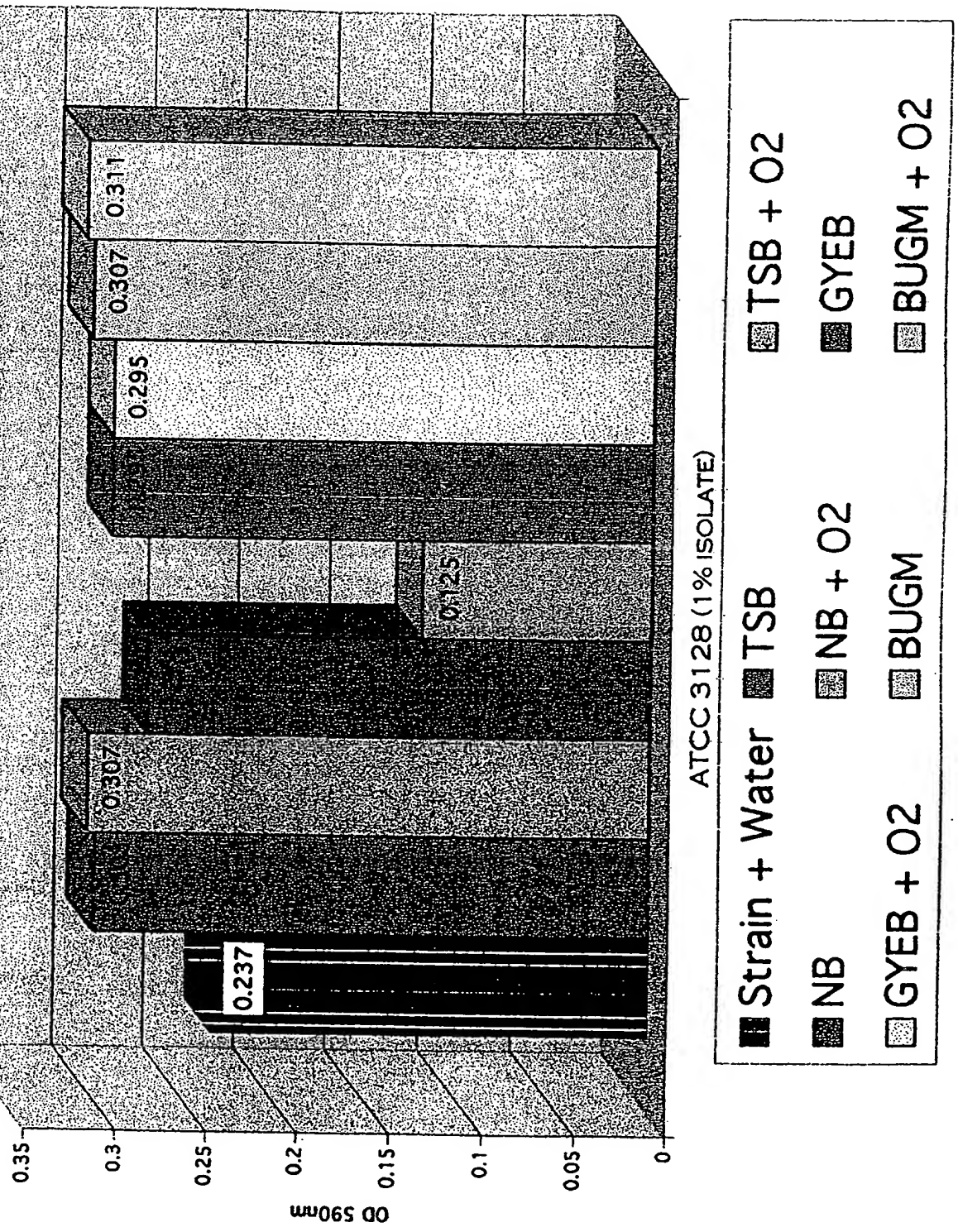

Minimal & Optimal Growth Temeratures for Selected Strains of Bacillus coagulans
Degrees Celsius
50
45
40
35
30
25
20
15
10
5
0
Minimal Growth Temperature
Optimal Growth Temperature
ATCC #31284 GYE
GBI-01 GYE
GBI-01 TSA
GBI-20 GYE
GBI-20 TSA
GBI-30 TSA
ATCC #31284 TSA

FIG. 2


OD 590nm
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
0.237
0.307
0.125
0.295
0.307
0.311
ATCC 3128 (1% ISOLATE)
Strain + Water
TSB
TSB + O2
NB
NB + O2
GYEB
GYEB + O2
BUGM
BUGM + O2

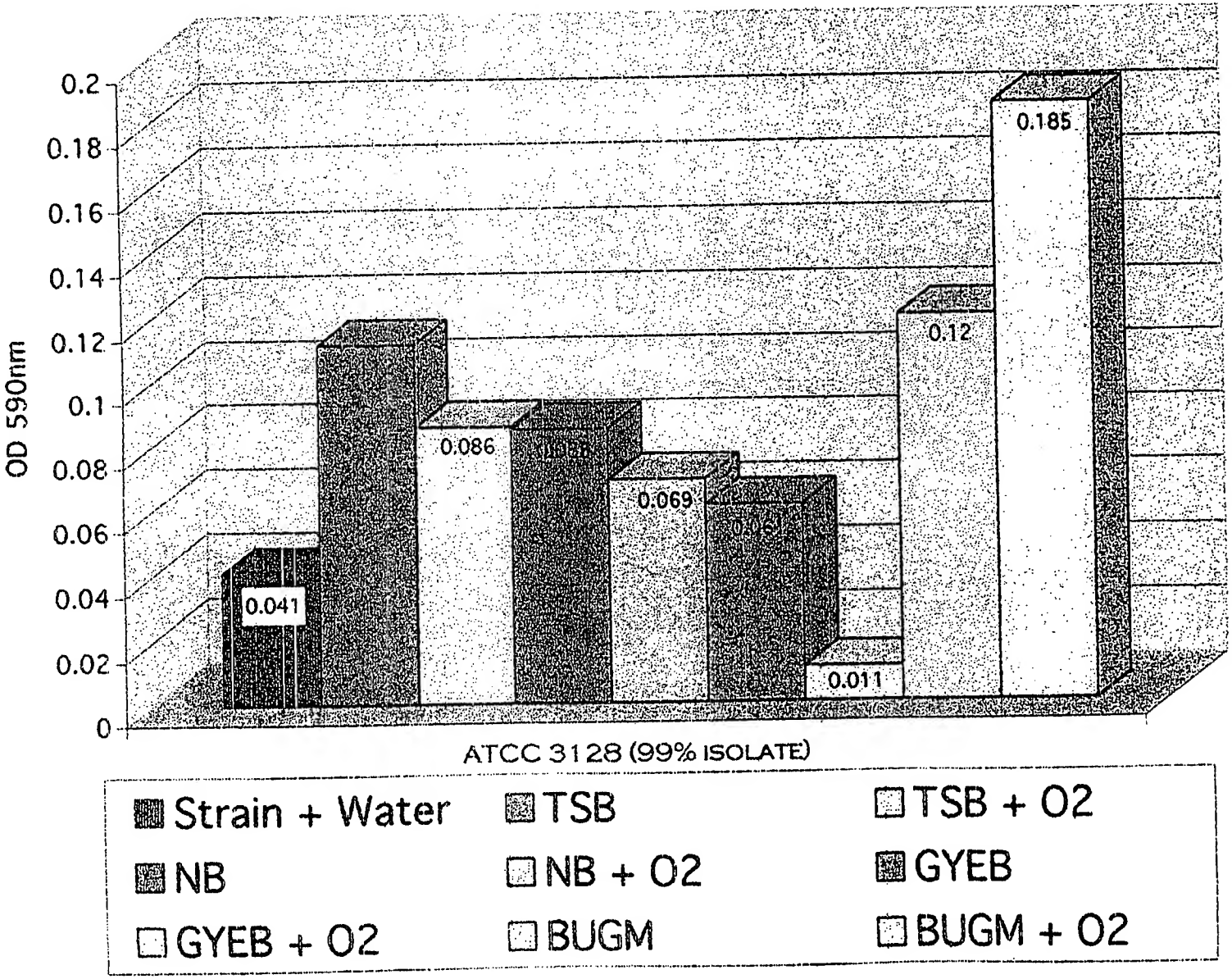

0.2
0.18
0.16
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
OD 590nm
0.041
0.086
0.069
0.011
0.12
0.185
ATCC 3128 (99% ISOLATE)
Strain + Water
TSB
TSB + O2
NB
NB + O2
GYEB
GYEB + O2
BUGM
BUGM + O2

FIG. 3

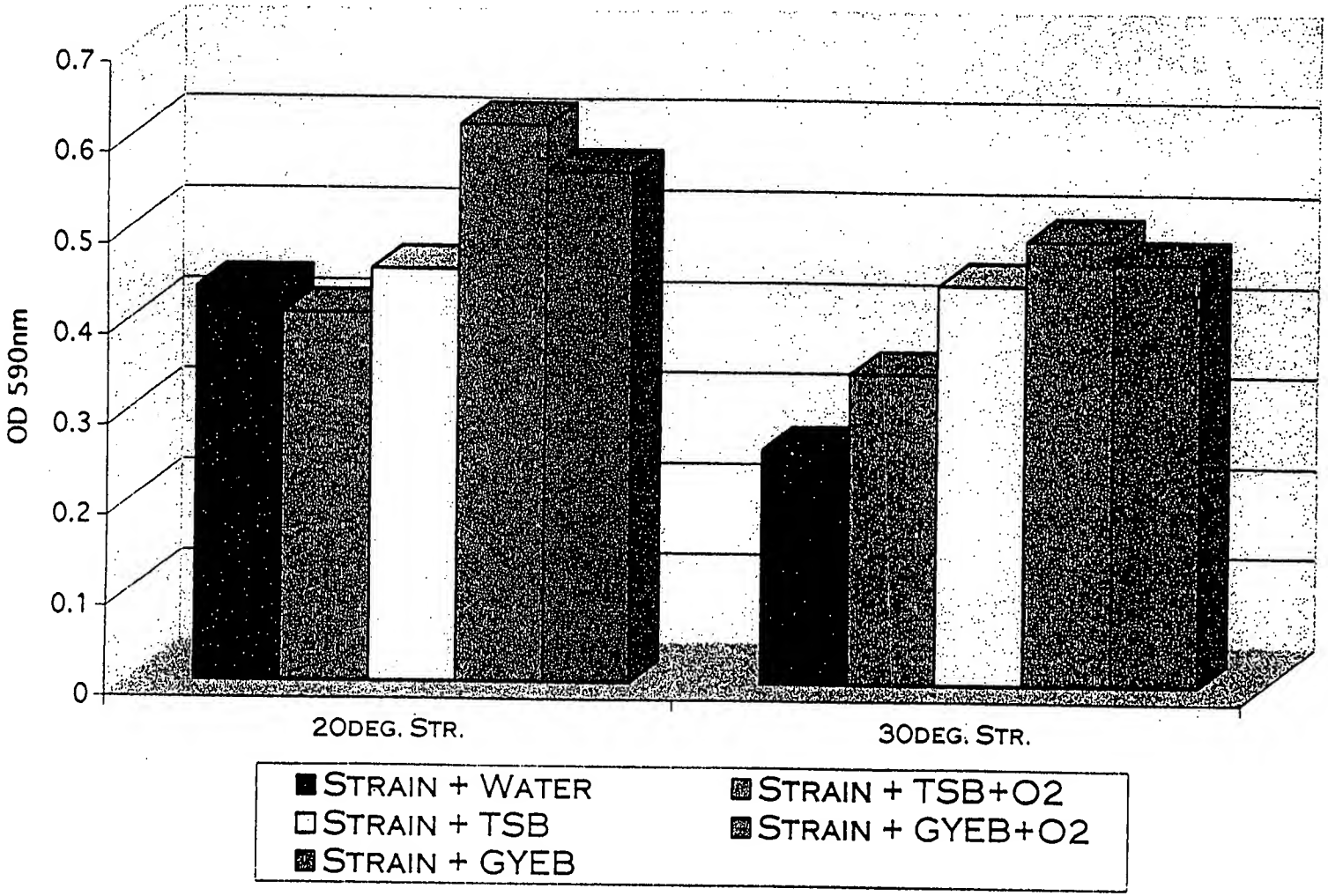

0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
OD 590nm
20DEG. STR.
30DEG. STR.
STRAIN + WATER
STRAIN + TSB
STRAIN + GYEB
STRAIN + TSB+O2
STRAIN + GYEB+O2

FIG. 4

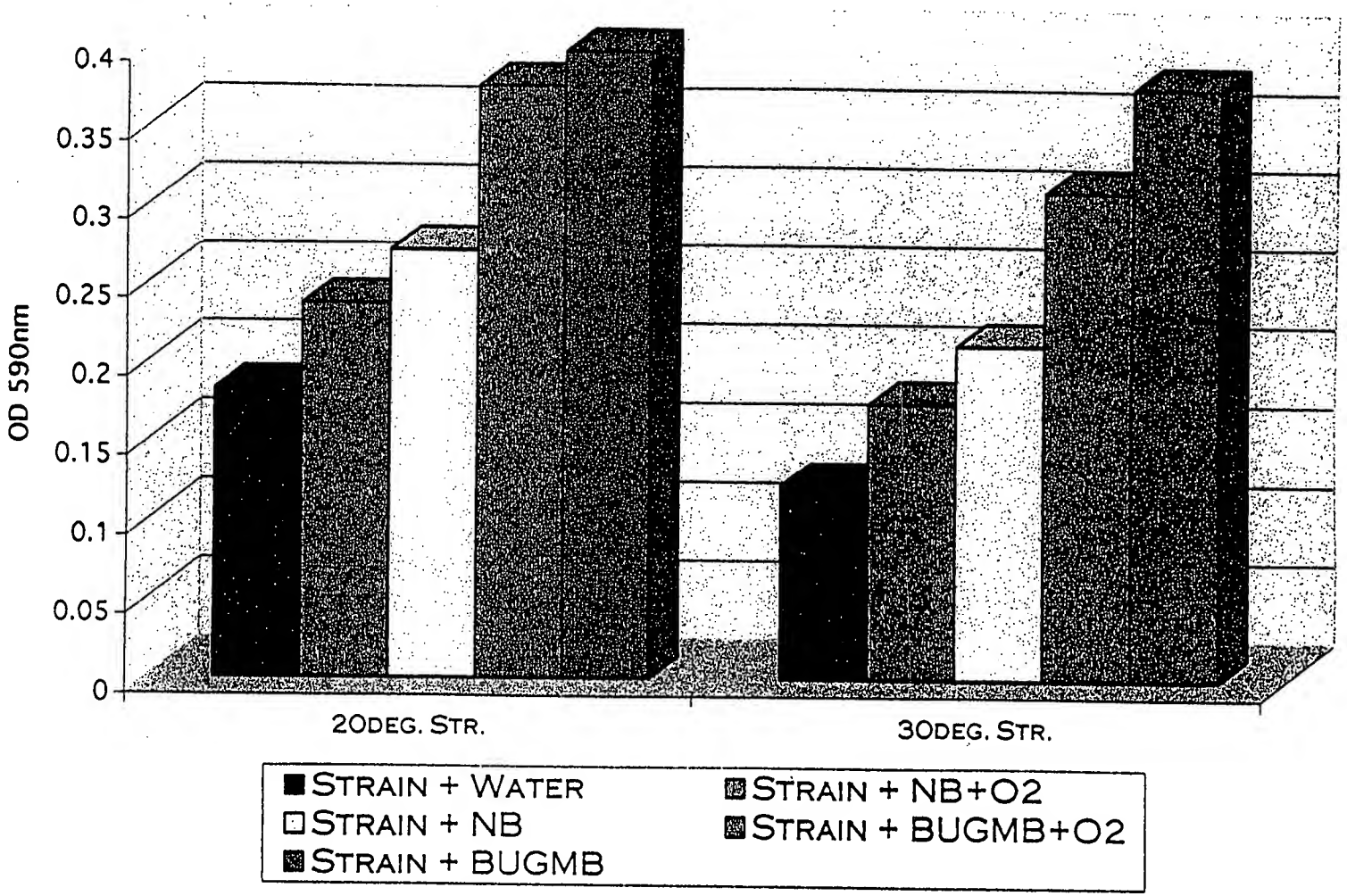
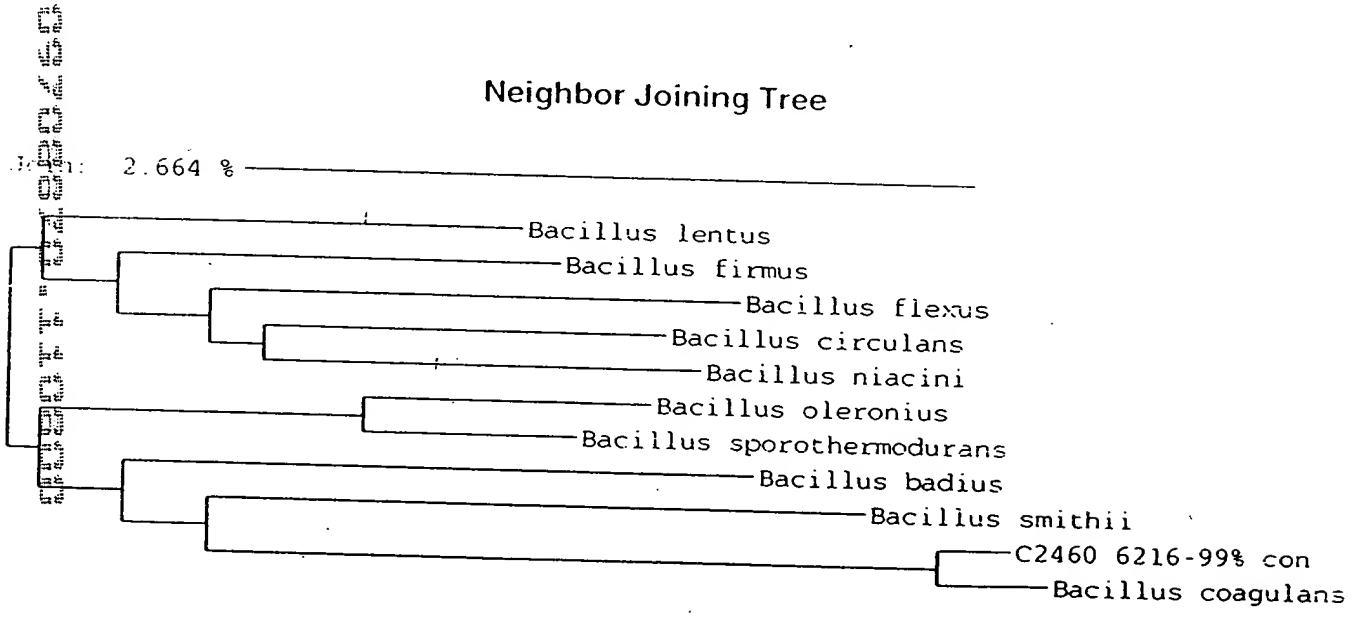

0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
OD 590nm
20DEG. STR.
30DEG. STR.
STRAIN + WATER
STRAIN + NB
STRAIN + BUGMB
STRAIN + NB+O2
STRAIN + BUGMB+O2

FIG. 5

FIG. 6

```
Alignment:  1549 C2460 6216-99% con
 0.65 % 1549 Bacillus coagulans
 4.84 % 1548 Bacillus oleronius
 5.36 % 1550 Bacillus smithii
 5.62 % 1548 Bacillus sporothermodurans
 5.65 % 1551 Bacillus badius
 5.79 % 1547 Bacillus firmus
 5.85 % 1547 Bacillus lentus
 5.90 % 1543 Bacillus circulans
 5.95 % 1545 Bacillus niacini
 6.30 % 1548 Bacillus flexus
```



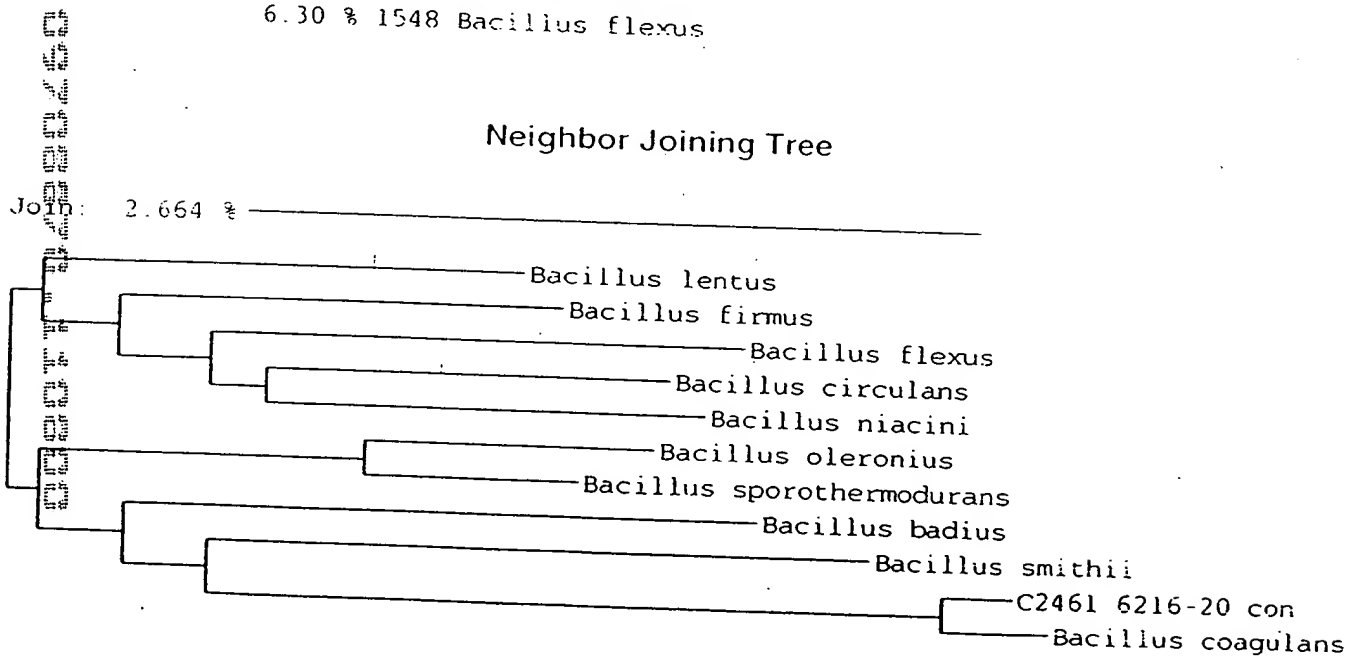
Concise Alignment

```
                    1
               111222222241
               347011256784
               902967240204
C2460 6216-99% con TCGAYTTWTTYC (SEQ ID NO:1; where r = A or G, y = C or T, and w = A or T)
Bacillus coagulans CTRGCGCACCCG (SEQ ID NO:2; where r = A or G, y = C or T, and w = A or T)
```

FIG. 7

```
Alignment:  1549 C2461 6216-20 con
 0.65 % 1549 Bacillus coagulans
 4.84 % 1548 Bacillus oleronius
 5.36 % 1550 Bacillus smithii
 5.62 % 1548 Bacillus sporothermodurans
 5.65 % 1551 Bacillus badius
 5.79 % 1547 Bacillus firmus
 5.85 % 1547 Bacillus lentus
 5.90 % 1543 Bacillus circulans
 5.95 % 1545 Bacillus niacini
 6.30 % 1548 Bacillus flexus
```

Neighbor Joining Tree



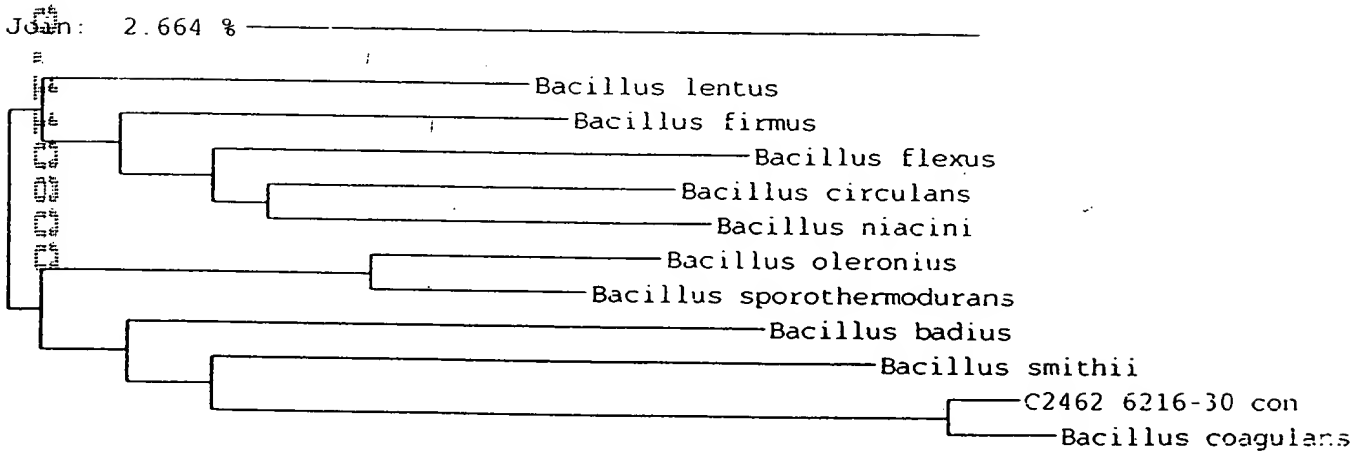
Concise Alignment

```
                          1
                 111222222241
                 347011256784
                 902967240204
C2461 6216-20 con TCGAYTTWTTYC  (SEQ ID NO:1; where r = A or G, y = C or T, and w = A or T)
Bacillus coagulans CTRGCGCACCCG  (SEQ ID NO:2; where r = A or G, y = C or T, and w = A or T)
```

FIG. 8

```
Alignment:  1549 C2462 6216-30 con
 0.65 % 1549 Bacillus coagulans
 4.84 % 1548 Bacillus oleronius
 5.36 % 1550 Bacillus smithii
 5.62 % 1548 Bacillus sporothermodurans
 5.65 % 1551 Bacillus badius
 5.79 % 1547 Bacillus firmus
 5.85 % 1547 Bacillus lentus
 5.90 % 1543 Bacillus circulans
 5.95 % 1545 Bacillus niacini
 6.30 % 1548 Bacillus flexus
```

Neighbor Joining Tree



Concise Alignment

```
                    1
               111222222241
               347011256784
               902967240204
C2462 6216-30 con  TCGAYTTWTTYC (SEQ ID NO:1; where r = A or G, y = C or T, and w = A or T)
Bacillus coagulans CTRGCGCACCCC (SEQ ID NO:2; where r = A or G, y = C or T, and w = A or T)
```

SCANNED, # 6

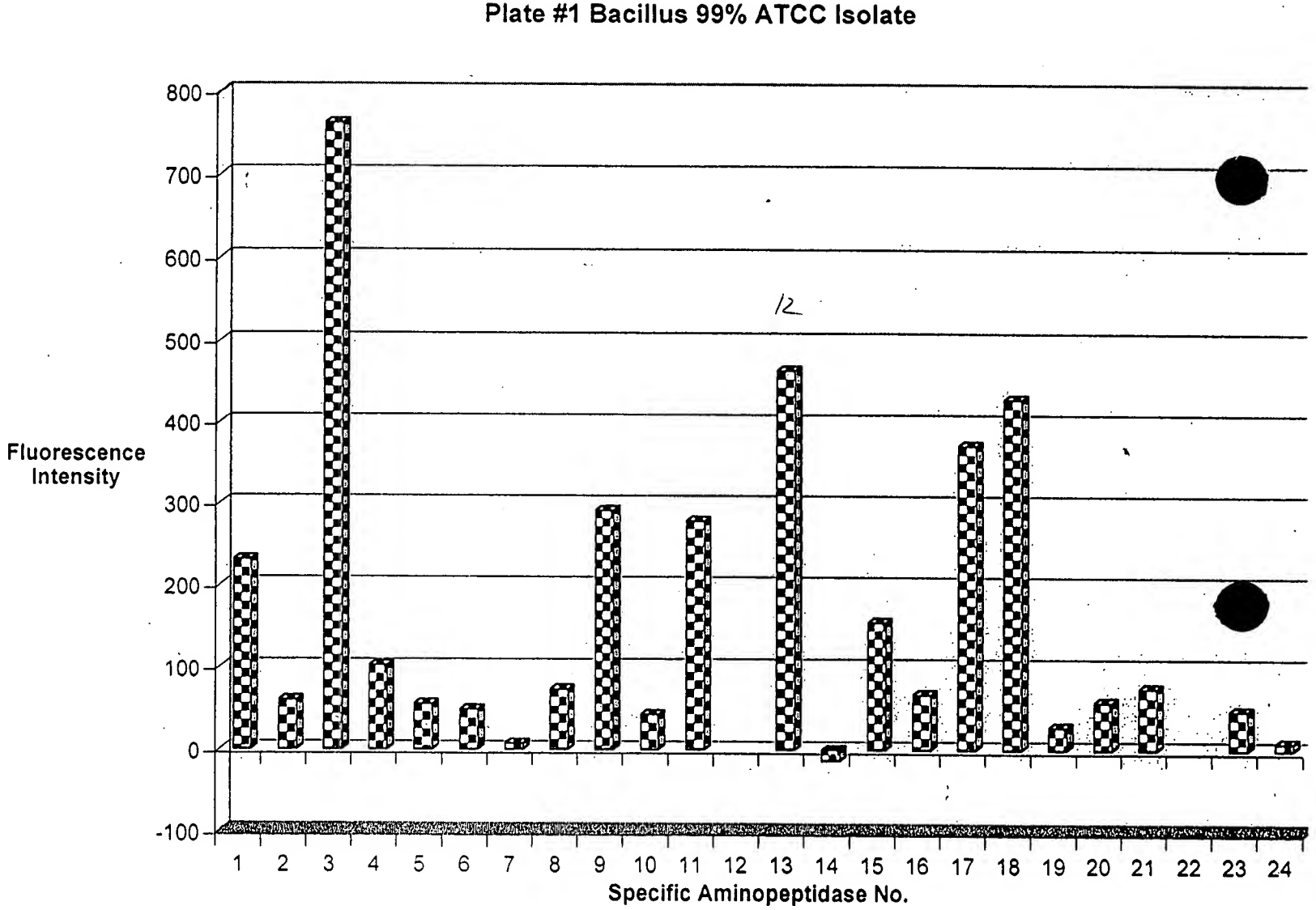


FIG. 9

SCANNED, # 6

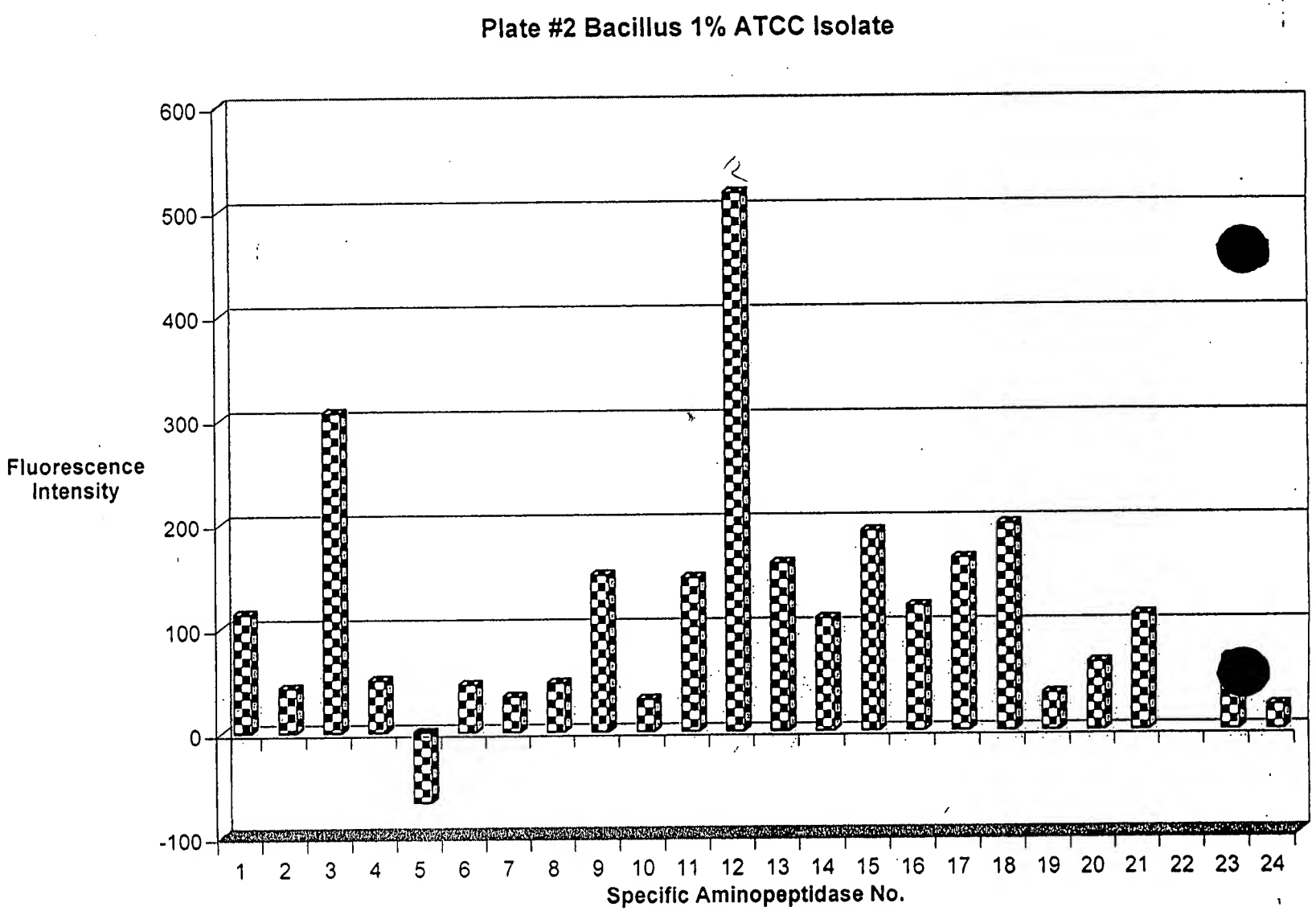


FIG. 10

SCANNED, #_6_

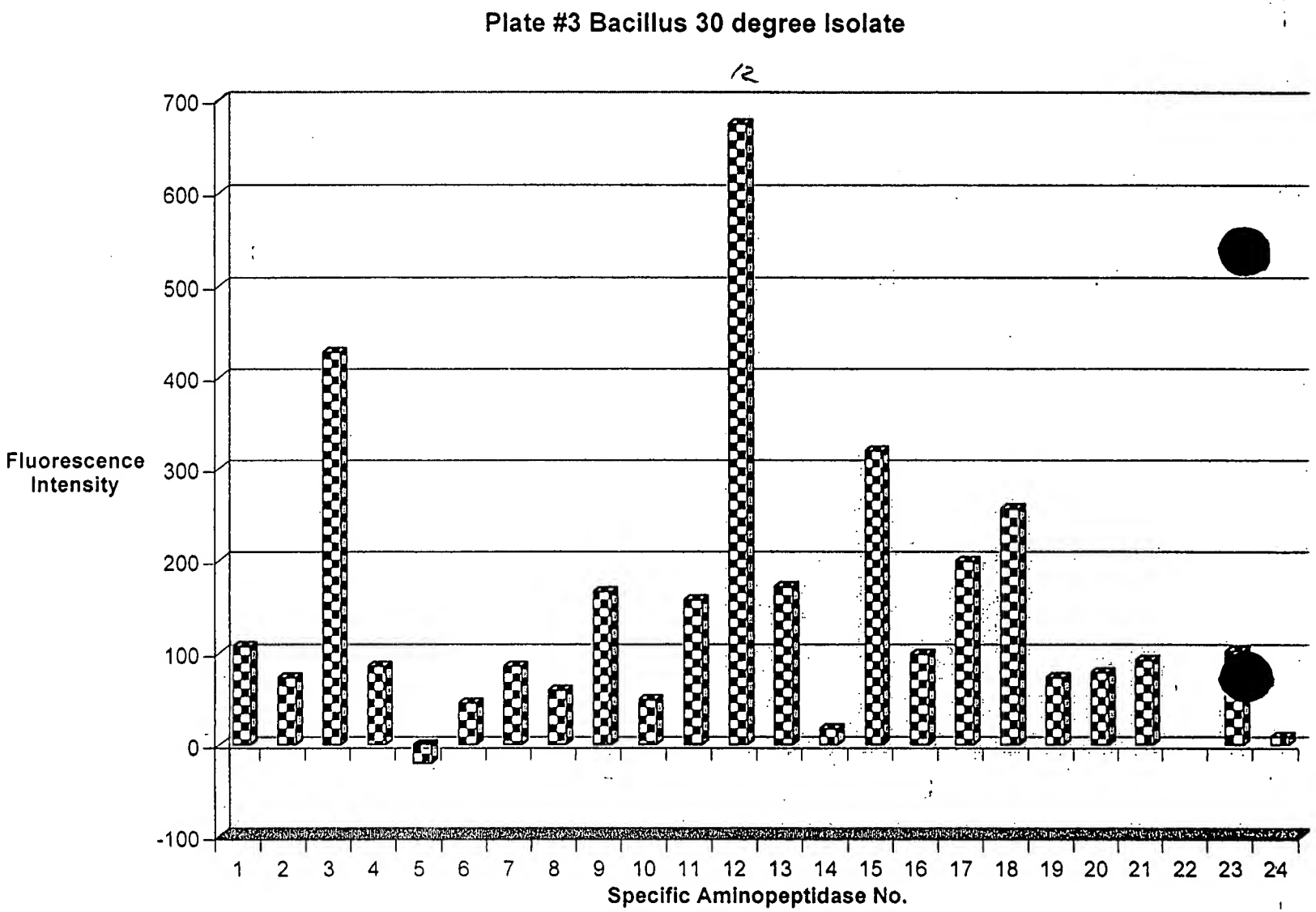


FIG. 11

SCANNED, # 6

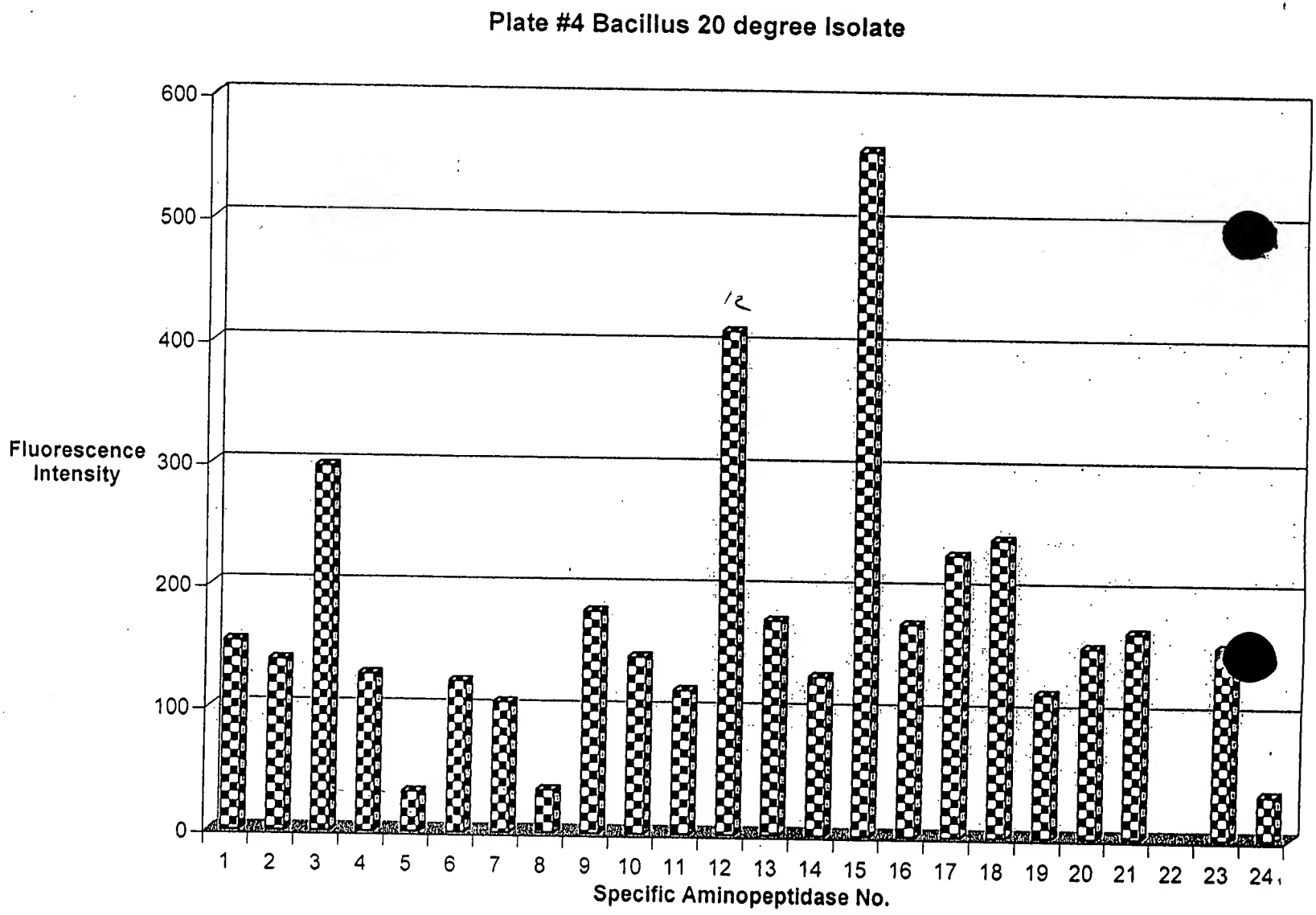


FIG. 12